STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 123751

To: Christopher Yaen
Location: REM/3A20/3C18
Art Unit: 1642
Wednesday, June 09, 2004

Case Serial Number: 09/538106

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Christopher,

This request was not forwarded to Ed Hart. It was placed in the "general pool" of incoming searches. I processed prior to reading CC: addressee.

Beverly

U.S. DEPARTMENT OF COMMERCE
Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's Name: ____________

Serial Number: ____________

Date: ____________

Phone: ____________

Art Unit: ____________

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

STAFF USE ONLY

Date completed: 06-09-04
Searcher: Beverly c 2528
Terminal time: ____________
Elapsed time: ____________
CPU time: ____________
Total time: ____________
Number of Searches: ____________
Number of Databases: ____________

Search Site

____ STIC
____ CM-1
____ Pre-S

Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
____ Bibliographic

Vendors

✓ IG
____ STN
____ Dialog
____ APS
____ Geninfo
____ SDC
____ DARC/Questel
____ Other

Yaen, C.
09/538106

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> O <
O| |O  IntelliGenetics
> O <

GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 9 Jun 104 10:05:27-PDT

Solution Parameters:

    Amino Alphabet      = Identity
    Output line length  = 80
    Compress            = Off
    Histogram           = Off
    Randomization       = Off

    AMINO-Res-length    = 2
    DELetion-weight     = 5.00
    LEngth-factor       = 0
    Matching-weight     = 1.00
    NUCLEIC-Res-length  = 4
    SPread-factor       = 50

Clustered order of selected sequences:

    13. US-09-538-106-24      (1-389)
     7. US-09-538-106-18      (1-393)
     4. US-09-538-106-15      (1-448)
    10. US-09-538-106-21      (1-483)
     6. US-09-538-106-17      (1-461)
    12. US-09-538-106-23      (1-461)
     3. US-09-538-106-14      (1-516)
     9. US-09-538-106-20      (1-555)
     8. US-09-538-106-19      (1-680)
     2. US-09-538-106-13      (1-641)
     5. US-09-538-106-16      (1-586)
    11. US-09-538-106-22      (1-586)
     1. s33377                (1-601)


Region Alignment: (listed in Clustered order)

US-09-538-    1

US-09-538-    1

US-09-538-    1

US-09-538-    1

US-09-538-    1                                                           MLY
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US-09-538-    1                                                           MLY

US-09-538-    1                                        MSQSTQTnEFLSPEVFQHIWDF
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US-09-538-    1 MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDF
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-    1 MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDF
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US-09-538-    1                                        MSQSTQTnEFLSPEVFQHIWDF

US-09-538-    1                                                           MLY
                                                                          |||
US-09-538-    1                                                           MLY

    s33377    1 mpsakqrgskgghgaaspsekgahpsggaddvakkpppapqqpppppaphpqqhpqqhpqn

 consensus      mnfetsrcatlqycpdpyiqrfietpahfswkesyyrsamsqstqt-eflspevfqhi---


US-09-538-    1

US-09-538-    1

US-09-538-    1

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US-09-538-    4 LE          NNAQTQFSE                          PQYTNLGLLNSMDQ
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US-09-538-    4 LE          NNAQTQFSE                          PQYTNLGLLNSMDQ
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US-09-538-   23 LEQPICSVQPIdLNFVDEPSEdGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
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US-09-538-   62 LEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
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US-09-538-   62 LEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
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US-09-538-   23 LEQPICSVQPIdLNFVDEPSEdGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
                ||               ||     ||                          |||||||||
US-09-538-    4 LE       NNAQTQFSEP   QYTN                          LGLLNSMDQ
                ||       ||||||||||   ||||                          |||||||||
US-09-538-    4 LE       NNAQTQFSEP   QYTN                          LGLLNSMDQ
                                                                    | |
    s33377   62 qahgkgghrggggggkssssssasaaaaaaaaasssascsrrlgralnflfyLaLvaaaaf

 consensus      leqpicsvqpi-lnfvdepse-gatnkieismdcirmqdsdlsdpmwpqytnlgllnsmdq


US-09-538-    1                        MLYLE          NNAQTQFSE
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US-09-538-    1                        MLYLE          NNAQTQFSE
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US-09-538-    1     MSQSTQTnEFLSPEVFQHIWDFLEQPICSVQPIdLNFVDEPSEdGATNKIEISMDCI
                    ||||||| ||||||||||||||||||||||||| ||||||||| |||||||||||||
US-09-538-   36 yrsaMSQSTQTsEFLSPEVFQHIWDFLEQPICSVQPIeLNFVDEPSEnGATNKIEISMDCI
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US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-   84 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-  123 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-  123 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-   84 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
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US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                                    |                     |               |
    s33377  123 sgwcvhhvleevqqvrrshqDfsrqreelgqglqgveqkvqsLqatfgtfesilrssqHkq

 consensus      qiqngssstqt-eflspyntdhaqnsvtapspyaqpsstfdalspspaipsntdypgphsf


US-09-538-   15             PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                            |||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   15             PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
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US-09-538-   58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   97 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                       |       |    |     ||                   | |   |
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-  139 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-  178 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
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US-09-538-  178 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
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US-09-538-  139 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
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US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                |          |     |  | ||   |                   |        |
    s33377  184 DltekavkqgeSevsriSevLqKLqneIlkdlsdgihvvkdarerdfTslentveeRltel
 consensus      dvsfqqsstaksatwtysteLkklycqIqngssstsaktcpiqikvmTpppqgavirampv

US-09-538-   64 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
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US-09-538-   64 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
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US-09-538-  119 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
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US-09-538-  158 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
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US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  192 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  231 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  231 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
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US-09-538-  192 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
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US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                 |                                            |       |
    s33377  245 tKsindniaiftevqkrsqkeindmkakvasleesegnkqdlkalkEavkeiqtSaksrew
 consensus      ykkaehvtevvkrcpnhelsrefnegqiappshlirvegnshaqyvedpitgrqsvlvpye

US-09-538-  125 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  125 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  180 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
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US-09-538-  219 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||         |        |        |     |            |    |    |
US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  253 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  292 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  292 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
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US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
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US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
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    s33377  306 dmealrstlqtmesdiytevrelvslkqeqqafkeaadterlaLqaltekllrseesvsrl
 consensus      ppqvgtefttvlynfmcnsscvggmnrrpiliivtletrdgqvlgrrcfearicacpgrdr

US-09-538-  186 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
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US-09-538-  241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
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US-09-538-  280 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
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US-09-538-  259 KADEDSIRKQQVSDStKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
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US-09-538-  259 KADEDSIRKQQVSDSaKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  314 KADEDSIRKQQVSDStKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  353 KADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  353 KADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
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US-09-538-  314 KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
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US-09-538-  259 KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  259 KADEDSIRKQQVSDSaKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                                                      |
    s33377  367 peeirrleeelrqlksdshgpkedggfrhseafealqqKsqgldsrlqhvedgvlsmqvas
 consensus      kadedsirkqqvsds-kngdgtkrpfrqnthgiqmtsikkrrspddellylpvrgretyem

US-09-538-  247 EARICACPGRDRKADEDSIRKQQVSDSaKNGD    aFRQNTHGIQMTSIKKRRSPDDELL
                ||||||||||||||||||||||||||| ||||     ||||||||||||||||||||||||
US-09-538-  247 EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  302 EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL
                ||||||||||||||||||||||||||| ||||     ||||||||||||||||||||||||
US-09-538-  341 EARICACPGRDRKADEDSIRKQQVSDSaKNGD    aFRQNTHGIQMTSIKKRRSPDDELL
                   |              |                             |
US-09-538-  320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSiQSpSSYGNSSPPLNKMNSMNK
                ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-  320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSmQSqSSYGNSSPPLNKMNSMNK
                ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-  375 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSiQSpSSYGNSSPPLNKMNSMNK
                ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-  414 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNK
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  414 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNK
                ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-  375 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNK
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNK
                ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-  320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSmQSqSSYGNSSPPLNKMNSMNK
                         |      |                   |    |
    s33377  428 arqteslesLlsksqeHeqrlapagaleglgsseadQdglaStvrslgetqlvlygdveel
 consensus      llkikeslelmqylpqhtietyrqqqqqqhqhllqkqts-qs-ssygnssplnkmnsmnk

US-09-538-  304 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  308 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
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US-09-538-  363 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  398 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
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US-09-538-  381 LPSVSQLINPQQRNALTPTTiPdGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
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US-09-538-  381 LPSVSQLINPQQRNALTPTTmPeGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-  436 LPSVSQLINPQQRNALTPTTiPdGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-  475 LPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  475 LPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
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                |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-  436 LPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  381 LPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-  381 LPSVSQLINPQQRNALTPTTmPeGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                  ||  |                             |        |
    s33377  489 krSVgeLpstveslqkvqeqvhtllsqdqaqaarlpPqdfldrlsSldnlkasvsqveadl

 consensus      lpsVsqlinpqqrnaltptt-p-gmganipmmgthmpmagdmnglsptqalppplsmpsts

US-09-538-  365 PRgEaPtQSDVFFRHSnPPNhSVYP
                || | | ||||||||| ||| ||||
US-09-538-  369 PRRETPKQSDVFFRHSKPPNRSVYP
                |||||||||||||||||||||||||
US-09-538-  424 PRRETPKQSDVFFRHSKPPNRSVYP
                || | | ||||||||| ||| ||||
US-09-538-  459 PRgEaPtQSDVFFRHSnPPNhSVYP
                     |
US-09-538-  442 HCTPPPPYPTDCSIV
                |||||||||||||||
US-09-538-  442 HCTPPPPYPTDCSIV
                |||||||||||||||
US-09-538-  497 HCTPPPPYPTDCSIV
                |||||||||||||||
US-09-538-  536 HCTPPPPYPTDCSIV
                |||||||||||||||
US-09-538-  536 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  497 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  442 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  442 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                              |
    s33377  550 kmlrtavdslvaysVkietnennlesakgllddlrndldrlfvkvekihekv

 consensus      hctppppyptdcsivsf--nl----cldyfttqglttiyqiehysmddlaslkipeqfrha

US-09-538-  390

US-09-538-  394

US-09-538-  449

US-09-538-  484

US-09-538-  457

US-09-538-  457

US-09-538-  512

US-09-538-  551

US-09-538-  597 IWKGILDHRQLHdFSSPpHLLRTPSgASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE
                |||||||||||| |||| ||||||| |||||||||||||||||||||||||||||||||||
US-09-538-  558 IWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  503 IWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE
                |||||||||||| |||| ||||||| |||||||||||||||||||||||||||||||||||
US-09-538-  503 IWKGILDHRQLHdFSSPpHLLRTPSgASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE

    s33377  602

 consensus      iwkgildhrqlh-fssp-hllrtps-astvsvgssetrgervidavrftlrqtisfpprde

US-09-538-  390

US-09-538-  394
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US-09-538-  449

US-09-538-  484

US-09-538-  457                 RIWQV
                                |||||
US-09-538-  457                 RIWQV
                                |||||
US-09-538-  512                 RIWQV
                                |||||
US-09-538-  551                 RIWQV
                                ||
US-09-538-  658 WNDFNFDMDsRRNKQQRIKEEGE
                ||||||||| |||||||||||||
US-09-538-  619 WNDFNFDMDARRNKQQRIKEEGE
                |||||||||||||||||||||||
US-09-538-  564 WNDFNFDMDARRNKQQRIKEEGE
                ||||||||| |||||||||||||
US-09-538-  564 WNDFNFDMDsRRNKQQRIKEEGE

    s33377  602

 consensus      wndfnfdmd-rrnkqqri---ge

Alignment score = -6012.00

Scoring matrix:

            1      2      3      4      5      6      7      8      9     10     11     12
      ------------------------------------------------------------------------------------
   1 |          -190   -399   -734    -75   -668  -1003   -366   -216   -554    -75   -668
   2 |                 -112   -548    293   -452   -888    434   -315   -769    292   -457
   3 |                          76   -314    168   -264   -315    313   -147   -321    171
   4 |                               -646    -44    108   -747   -123    219   -648    -54
   5 |                                      -167   -603     97   -148   -462    577   -172
   6 |                                               21   -652    -24    -91   -172    456
   7 |                                                    -1084   -460   -118   -604     20
   8 |                                                            -73   -529    106   -647
   9 |                                                                    91   -148    -19
  10 |                                                                          -469    -91
  11 |                                                                                 -167
  12 |
  13 |


           13
      -------
   1 |  -1019
   2 |   -911
   3 |   -289
   4 |     77
```

```
 5 |  -626
 6 |    -4
 7 |   362
 8 | -1103
 9 |  -483
10 |   -91
11 |  -623
12 |    -3
13 |

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```

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> O <
O| |O  IntelliGenetics
> O <

GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 9 Jun 104 10:07:05-PDT

Solution Parameters:

    Amino Alphabet     = Identity
    Output line length = 80
    Compress           = Off
    Histogram          = Off
    Randomization      = Off

    AMINO-Res-length   = 2
    DELetion-weight    = 5.00
    LEngth-factor      = 0
    Matching-weight    = 1.00
    NUCLEIC-Res-length = 4
    SPread-factor      = 50

Clustered order of selected sequences:

    13. US-09-538-106-24      (1-389)
     7. US-09-538-106-18      (1-393)
     4. US-09-538-106-15      (1-448)
    10. US-09-538-106-21      (1-483)
     6. US-09-538-106-17      (1-461)
    12. US-09-538-106-23      (1-461)
     3. US-09-538-106-14      (1-516)
     9. US-09-538-106-20      (1-555)
     8. US-09-538-106-19      (1-680)
     2. US-09-538-106-13      (1-641)
     5. US-09-538-106-16      (1-586)
    11. US-09-538-106-22      (1-586)
    22. caa49535              (1-602)


Region Alignment: (listed in Clustered order)

US-09-538-    1

US-09-538-    1

US-09-538-    1

US-09-538-    1

US-09-538-    1                                                           MLY
                                                                          |||
US-09-538-    1                                                           MLY

US-09-538-    1                                        MSQSTQTnEFLSPEVFQHIWDF
                                                       ||||||| ||||||||||||||
US-09-538-    1 MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDF
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-    1 MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDF
                                                       ||||||| ||||||||||||||
US-09-538-    1                                        MSQSTQTnEFLSPEVFQHIWDF

US-09-538-    1                                                           MLY
                                                                          |||
US-09-538-    1                                                           MLY

   caa49535   1 mpsakqrgskgghgaaspsekgahpsggaddvakkpppapqqpppppaphpqqhpqqhpqn

  consensus     mnfetsrcatlqycpdpyiqrfietpahfswkesyyrsamsqstqt-eflspevfqhi---
```

```
US-09-538-    1
US-09-538-    1
US-09-538-    1
US-09-538-    1                           mnfetsrcatlqycpdpyiqrfieTpahfswkesy
                                                                  |
US-09-538-    4 LE          NNAQTQFSE                          PQYTNLGLLNSMDQ
                ||          |||||||||                          ||||||||||||||
US-09-538-    4 LE          NNAQTQFSE                          PQYTNLGLLNSMDQ
                ||           |     ||                          ||||||||||||||
US-09-538-   23 LEQPICSVQPIdLNFVDEPSEdGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
                ||||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||||
US-09-538-   62 LEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   62 LEQPICSVQPIELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
                ||||||||||| ||||||||| |||||||||||||||||||||||||||||||||||||||
US-09-538-   23 LEQPICSVQPIdLNFVDEPSEdGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQ
                ||               ||     ||                          |||||||||
US-09-538-    4 LE       NNAQTQFSEP   QYTN                          LGLLNSMDQ
                ||       ||||||||||   ||||                          |||||||||
US-09-538-    4 LE       NNAQTQFSEP   QYTN                          LGLLNSMDQ
                                                                    | |
caa49535     62 qahgkgghrggggggkssssssasaaaaaaaaasssascsrrlgralnflfyLaLvaaaaf
consensus       leqpicsvqpi-lnfvdepse-gatnkieismdcirmqdsdlsdpmwpqytnlgllnsmdq

US-09-538-    1                        MLYLE          NNAQTQFSE
                                       |||||          |||||||||
US-09-538-    1                        MLYLE          NNAQTQFSE
                                          ||           |     ||
US-09-538-    1     MSQSTQTnEFLSPEVFQHIWDFLEQPICSVQPIdLNFVDEPSEdGATNKIEISMDCI
                    ||||||| ||||||||||||||||||||||||| ||||||||| |||||||||||||
US-09-538-   36 yrsaMSQSTQTsEFLSPEVFQHIWDFLEQPICSVQPIeLNFVDEPSEnGATNKIEISMDCI
                     | ||      ||    |       |    ||        ||     |
US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   84 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  123 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  123 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   84 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                |||||||||      ||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   29 QIQNGSSST      SPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSF
                                    |                     |               |
caa49535    123 sgwcvhhvleevqqvrrshqDfsrqreelgqglqgveqkvqsLqatfgtfesilrssqHkq
consensus       qiqngssstqt-eflspyntdhaqnsvtapspyaqpsstfdalspspaipsntdypgphsf

US-09-538-   15             PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                            |||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   15             PQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                            |||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   58 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   97 RMQDSDLSDPMWPQYTNLGLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFD
                       |       |    |     ||                   | |   |
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-  139 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-  178 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
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                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-  178 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-  139 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                ||||||||||||||||||||||||||||        |||||||||||||||||||||||||
US-09-538-   84 DVSFQQSSTAKSATWTYSTELKKLYCQI        AKTCPIQIKVMTPPPQGAVIRAMPV
                |          |     |  | ||   |                   |        |
caa49535    184 DltekavkqgeSevsriSevLqKLqneIlkdlsdgihvvkdarerdfTslentveeRltel
consensus       dvsfqqsstaksatwtysteLkklycqIqngssstsaktcpiqikvmTpppqgavirampv

US-09-538-   64 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   64 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  119 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  158 ALSPSPAIPSNTDYPGPHSFDVSFQQSSTAKSATWTYSTELKKLYCQIAKTCPIQIKVMTP
                              |                |            |     |      |
US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  192 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  231 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  231 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  192 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  137 YKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYE
                 |                                            |       |
caa49535    245 tKsindniaiftevqkrsqkeindmkakvasleesegnkqdlkalkEavkeiqtSaksrew
consensus       ykkaehvtevvkrcpnhelsrefnegqiappshlirvegnshaqyvedpitgrqsvlvpye

US-09-538-  125 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  125 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  180 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  219 PPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDP
                |||         |        |        |     |            |    |    |
US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  253 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  292 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  292 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  253 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-  198 PPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFEARICACPGRDR
                                                           |
caa49535    306 dmealrstlqtmesdiytevrelvslkqeqqafkeaadterlaLqaltekllrseesvsrl
consensus       ppqvgtefttvlynfmcnsscvggmnrrpiliivtletrdgqvlgrrcfearicacpgrdr

US-09-538-  186 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
```

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                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   186 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   241 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   280 ITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCF
                      |               |                         |
US-09-538-   259 KADEDSIRKQQVSDStKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   259 KADEDSIRKQQVSDSaKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   314 KADEDSIRKQQVSDStKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   353 KADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   353 KADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   314 KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   259 KADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                 ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   259 KADEDSIRKQQVSDSaKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEM
                                                       |
  caa49535   367 peeirrleeelrqlksdshgpkedggfrhseafealqqKsqgldsrlqhvedgvlsmqvas

 consensus       kadedsirkqqvsds-kngdgtkrpfrqnthgiqmtsikkrrspddellylpvrgretyem


US-09-538-   247 EARICACPGRDRKADEDSIRKQQVSDSaKNGD    aFRQNTHGIQMTSIKKRRSPDDELL
                 ||||||||||||||||||||||||||| ||||     ||||||||||||||||||||||||
US-09-538-   247 EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   302 EARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELL
                 ||||||||||||||||||||||||||| ||||     ||||||||||||||||||||||||
US-09-538-   341 EARICACPGRDRKADEDSIRKQQVSDSaKNGD    aFRQNTHGIQMTSIKKRRSPDDELL
                    |              |                             |
US-09-538-   320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSiQSpSSYGNSSPPLNKMNSMNK
                 ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-   320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSmQSqSSYGNSSPPLNKMNSMNK
                 ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-   375 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSiQSpSSYGNSSPPLNKMNSMNK
                 ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-   414 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNK
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   414 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNK
                 ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-   375 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNK
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNK
                 ||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||||
US-09-538-   320 LLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKQTSmQSqSSYGNSSPPLNKMNSMNK
                          |      |       |                           |
  caa49535   428 arqteslesLlsksqeHeqrlaalQgrleglgsseadqdglastvrslgetqLvlygdvee

 consensus       llkikeslelmqylpqhtietyrqqqqqqhqhllqkqts-qs-ssygnssplnkmnsmnk


US-09-538-   304 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   308 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   363 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   398 YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQHLLQKHLLSACFRNELVE
                    |                                        |     |
US-09-538-   381 LPSVSQLINPQQRNALTPTTiPdGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-   381 LPSVSQLINPQQRNALTPTTmPeGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-   436 LPSVSQLINPQQRNALTPTTiPdGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-   475 LPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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US-09-538-   475 LPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-   436 LPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   381 LPSVSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
US-09-538-   381 LPSVSQLINPQQRNALTPTTmPeGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
                 |                                   |       ||    |    |
  caa49535   489 LkrsvgelpstveslqkvqeqvhtllsqdqaqaarlPpqdfldrLSsldnLkasvSqvead

 consensus       lpsvsqlinpqqrnaltptt-p-gmganipmmgthmpmagdmngLsptqaLppplsmpsts


US-09-538-   365 PRgEaPtQSDVFFRHSnPPNhSVYP
                 || | | ||||||||| ||| ||||
US-09-538-   369 PRRETPKQSDVFFRHSKPPNRSVYP
                 |||||||||||||||||||||||||
US-09-538-   424 PRRETPKQSDVFFRHSKPPNRSVYP
                 || | | ||||||||| ||| ||||
US-09-538-   459 PRgEaPtQSDVFFRHSnPPNhSVYP
                      |
US-09-538-   442 HCTPPPPYPTDCSIV
                 |||||||||||||||
US-09-538-   442 HCTPPPPYPTDCSIV
                 |||||||||||||||
US-09-538-   497 HCTPPPPYPTDCSIV
                 |||||||||||||||
US-09-538-   536 HCTPPPPYPTDCSIV
                 |||||||||||||||
US-09-538-   536 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   497 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   442 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   442 HCTPPPPYPTDCSIVSFLARLGCSSCLDYFTTQGLTTIYQIEHYSMDDLASLKIPEQFRHA
                                                   |
  caa49535   550 lkmlrtavdslvaysvkietnennlesakglldd Lrndldrlfvkvekihekv

 consensus       hctppppyptdcsivsf---l----cldyfttqglttiyqiehysmddlaslkipeqfrha


US-09-538-   390

US-09-538-   394

US-09-538-   449

US-09-538-   484

US-09-538-   457

US-09-538-   457

US-09-538-   512

US-09-538-   551

US-09-538-   597 IWKGILDHRQLHdFSSPpHLLRTPSgASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE
                 |||||||||||| |||| ||||||| |||||||||||||||||||||||||||||||||||
US-09-538-   558 IWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE
                 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-538-   503 IWKGILDHRQLHEFSSPSHLLRTPSSASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE
                 |||||||||||| |||| ||||||| |||||||||||||||||||||||||||||||||||
US-09-538-   503 IWKGILDHRQLHdFSSPpHLLRTPSgASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDE

  caa49535   603

 consensus       iwkgildhrqlh-fssp-hllrtps-astvsvgssetrgervidavrftlrqtisfpprde


US-09-538-   390
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US-09-538-  394

US-09-538-  449

US-09-538-  484

US-09-538-  457                 RIWQV
                                |||||
US-09-538-  457                 RIWQV
                                |||||
US-09-538-  512                 RIWQV
                                |||||
US-09-538-  551                 RIWQV
                                ||
US-09-538-  658 WNDFNFDMDsRRNKQQRIKEEGE
                ||||||||| |||||||||||||
US-09-538-  619 WNDFNFDMDARRNKQQRIKEEGE
                |||||||||||||||||||||||
US-09-538-  564 WNDFNFDMDARRNKQQRIKEEGE
                ||||||||| |||||||||||||
US-09-538-  564 WNDFNFDMDsRRNKQQRIKEEGE

  caa49535  603

 consensus      wndfnfdmd-rrnkqqri---ge

Alignment score = -6009.00

Scoring matrix:

       22     2     3     4     5     6     7     8     9    10    11    12
    ------------------------------------------------------------------------
22 |        -185  -404  -739   -80  -673 -1008  -356  -221  -558   -80  -673
 2 |              -112  -548   293  -452  -888   434  -315  -769   292  -457
 3 |                      76  -314   168  -264  -315   313  -147  -321   171
 4 |                          -646   -44   108  -747  -123   219  -648   -54
 5 |                                -167  -603    97  -148  -462   577  -172
 6 |                                        21  -652   -24   -91  -172   456
 7 |                                            -1084  -460  -118  -604    20
 8 |                                                    -73  -529   106  -647
 9 |                                                           91  -148   -19
10 |                                                                -469   -91
11 |                                                                      -167
12 |
13 |

       13
    -------
22 | -1024
 2 |  -911
 3 |  -289
```

```
 4 |    77
 5 |  -626
 6 |    -4
 7 |   362
 8 | -1103
 9 |  -483
10 |   -91
11 |  -623
12 |    -3
13 |

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```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file caa49535.res made by bshears on Wed 9 Jun 104 10:10:28-PDT.


Query sequence being compared:    caa49535 (1-602)
Number of sequences searched:                   12
Number of scores above cutoff:                  12

      Results of the initial comparison of caa49535 (1-602) with:
        File : /home/bshears/new.pep

   100-
      -
N     -
U   50-
M     -
B     -
E     -
R     -
      -
O     -
F   10-
      -
S     -
E    5-                                          *       *
Q     -
U     -                                                           *
E     -
N     -
C     -
E     -
S    0-----------------------------------------------------------------
      ||     |  |   |   | |      |     |  |   |   |  |     |      |
SCORE 0|     1  |   2   | 2      3     4  |   5   |  5     6      7
STDEV -5       -4      -2      -1         0       1


                              PARAMETERS

Similarity matrix      Unitary    K-tuple                    2
Mismatch penalty             1    Joining penalty           20
Gap penalty               1.00    Window size               32
Gap size penalty          0.05
Cutoff score                 0
Randomization group          0

                              SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            5          7            0.83

Times:                   CPU                     Total Elapsed
                      00:00:00.00                00:00:00.00

Number of residues:                 6199
Number of sequences searched:         12
Number of scores above cutoff:        12


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.


The list of best scores is:
```

```
                                                                Init. Opt.
Sequence Name     Description                            Length Score Score  Sig. Frame
-----------------------------------------------------------------------------------------
                   ****  2 standard deviations above mean ****
  1. US-09-538-106-24 Sequence 24, Application     389     7  .  61   2.40   0
  2. US-09-538-106-18 Sequence 18, Application     393     7     61   2.40   0
  3. US-09-538-106-15 Sequence 15, Application     448     7     66   2.40   0
                   ****  1 standard deviation above mean ****
  4. US-09-538-106-22 Sequence 22, Application     586     6     77   1.20   0
  5. US-09-538-106-16 Sequence 16, Application     586     6     78   1.20   0
  6. US-09-538-106-13 Sequence 13, Application     641     6     78   1.20   0
  7. US-09-538-106-19 Sequence 19, Application     680     6     77   1.20   0
                   ****  0 standard deviation from mean ****
  8. US-09-538-106-23 Sequence 23, Application     461     5     28   0.00   0
  9. US-09-538-106-17 Sequence 17, Application     461     5     28   0.00   0
 10. US-09-538-106-21 Sequence 21, Application     483     5     79   0.00   0
 11. US-09-538-106-14 Sequence 14, Application     516     5     74   0.00   0
 12. US-09-538-106-20 Sequence 20, Application     555     5     74   0.00   0


1. caa49535 (1-602)
   US-09-538-106-24 Sequence 24, Application US/09538106

 Sequence 24, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 24
   LENGTH: 389
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score    =      7  Optimized Score  =      61  Significance =  2.40
Residue Identity =    18%  Matches          =      80  Mismatches   =   281
Gaps             =     65  Conservative Substitutions               =     0

            10        20        30        40    X   50        60        70
    MPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGG
                                                        |     ||    |
                                                MLYLENNAQTQFSEPQYTNLGLLNSMDQ
                                                X       10        20

           80         90       100       110       120       130       140
    GGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQ
        | || |      |     | |  |  |     ||      |        |   |      ||
    QIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKS
    30        40        50         60          70          80         90

         150       160       170           180         190       200
    DFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQ
           ||   |     |    |    |       |      |     ||        | ||     |
    ATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
      100        110       120       130       140       150       160

   210                   220       230       240       250       260
    NEIL------------KDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIFTEVQKRSQKEIND
       |             |   |   |    |      | |     | |      |         |    |
```

```
   PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----TVL-YNFMCNSSCVGGMNRRPILII--
    170       180       190       200             210       220       230

  270       280       290       300       310       320       330
   MKAKVASLEESEGNKQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFK-
          ||   |  | |                |  |    |              |      |     |
   -----VTLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDAFRQNTHGIQMTSIKKR
                 240       250       260       270       280       290

 340           350       360       370       380       390       400
   EAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQKSQ
      | | | |        | ||   ||            |  ||     |                | ||
   RSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH--------------QHLLQK--
     300       310       320       330       340                     350

   410          420       430       440 X     450       460       470
   GLDS---RLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSLG
    | |   |   ||               |     |
   HLLSACFRNELVEPRGEAPTQSDVFFRHSNPPNHSVYP
         360       370       380        X

    480       490
   ETQLVLYGDVEELKRS


2. caa49535 (1-602)
   US-09-538-106-18 Sequence 18, Application US/09538106

 Sequence 18, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 18
   LENGTH: 393
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score       =      7  Optimized Score    =      61  Significance =  2.40
Residue Identity    =    19%  Matches            =      83  Mismatches   =   278
Gaps                =     69  Conservative Substitutions             =     0

            10        20        30        40   X    50        60        70
   MPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGG
                                                       |     ||    |
                                               MLYLENNAQTQFSEPQYTNLGLLNSMDQ
                                               X        10        20

          80          90        100       110       120       130       140
   GGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQ
       | || |      |     | |  |  |     ||      |        |   |      ||
   QIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKS
   30        40        50         60          70          80        90

        150        160       170           180         190       200
   DFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQ
          ||   |     |    |    |       |      |     ||        | ||     |
   ATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
```

```
     100       110        120       130       140       150       160

  210                   220       230       240       250       260
   NEIL------------KDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIFTEVQKRSQKEIND
      |             |   |   |    |      | |     | |      |         |    |
   PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----TVL-YNFMCNSSCVGGMNRRPILII--
    170       180       190       200             210       220       230

  270       280        290         300       310       320        330
   MKAKVASLEESEGNKQDL-KALKEA--VKEIQTSAKSREWDMEALRSTLQTMESD-IYTEVRELVSLKQEQQ
          ||   |  | |     ||          |  |           |   |      |      |
   -----VTLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTS
                 240       250       260       270       280       290

     340           350       360       370       380       390       400
   AFK-EAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQ
     |    | | | |        | ||   ||            |  ||     |                |
   IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH--------------QHLL
     300       310       320       330       340                     350

       410          420       430       440 X     450       460       470
   QKSQGLDS---RLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTV
   ||   | |   |   ||               |     |
   QK--HLLSACFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
         360       370       380       390  X

        480       490
   RSLGETQLVLYGDVEELKRS


3. caa49535 (1-602)
   US-09-538-106-15 Sequence 15, Application US/09538106

 Sequence 15, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
   LENGTH: 448
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score       =      7  Optimized Score    =      66  Significance =  2.40
Residue Identity    =    18%  Matches            =      93  Mismatches   =   296
Gaps                =    101  Conservative Substitutions             =     0

              X                   10        20            30         40
              MPSAKQ------------RGSKGGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPP
               |   |                       ||| ||      |             |  |
   MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQY
           10 X      20        30        40        50        60        70

       50       60        70        80          90       100       110
   PPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLA
             ||  ||               | || |      |     | |  |  |     ||      |
   TNLGLLNSMDQQ-IQN---------------GSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPA
         80                        90       100       110        120
```

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      120       130       140       150       160       170           180
    LVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK-
            |   |      ||             ||   |     |    |    |       |      |
    IPSNTDYPG--PHSFDVSFQQSSTAKSATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKK
      130         140       150        160       170       180       190

          190       200       210                   220       230       240
    -QDLTEKAVKQGESEVSRISEVLQKLQNEIL------------KDLSDGIHVVKDARERDFTSLENTVEERL
        ||        | ||     |      |             |   |   |    |      | |
    AEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----
       200       210       220       230       240       250       260

          250       260       270       280        290         300       310
    TELTKSINDNIAIFTEVQKRSQKEINDMKAKVASLEESEGNKQDL-KALKEA--VKEIQTSAKSREWDMEAL
    | |      |         |    |         ||   |  | |     ||          |  |
    TVL-YNFMCNSSCVGGMNRRPILII-------VTLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQ
           270       280              290         300       310       320

           320        330        340           350       360       370
    RSTLQTMESD-IYTEVRELVSLKQEQQAFK-EAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEE
         |   |      |      |     |    | | | |        | ||   ||            |
    QVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIET
        330       340       350       360       370       380       390

     380       390       400       410          420       430       440 X
    LRQLKSDSHGPKEDGGFRHSEAFEALQQKSQGLDS---RLQHVEDGVLSMQVASARQTESLESLLSKSQEHE
     ||     |                | ||   | |   |   ||               |     |
    YRQQQQQQH--------------QHLLQK--HLLSACFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
      400                     410         420       430       440       X

      450       460       470       480       490
    QRLAALQGRLEGLGSSEADQDGLASTVRSLGETQLVLYGDVEELKRS
```

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4. caa49535 (1-602)
   US-09-538-106-22 Sequence 22, Application US/09538106

 Sequence 22, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
   LENGTH: 586
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score    =      6  Optimized Score  =     77  Significance =  1.20
Residue Identity =    19%  Matches          =    111  Mismatches   =   343
Gaps             =    119  Conservative Substitutions              =     0

                                                      X          10
                                                      MPS---AKQRGSKGGHGAASPS
                                                       ||        |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
            30        40        50        60        70        80        90
```

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   20              30        40        50        60            70       80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
         100       110       120                130       140       150

          90       100       110       120       130                    140
    SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
      160              170         180       190       200       210

          150                160       170       180       190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVL
          |  |         || | |         |  |        |  ||     | | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDSA-KNG------DGTKR
   220       230       240        250       260       270              280

       210         220       230       240                 250        260
    QKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQKRSQ
       ||        ||     |  |  |   |   |  | |   | |               | |   |   |
    PFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQ
               290       300       310       320       330       340

        270       280        290       300       310       320       330
    KEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
          |        | ||    |       |    |         ||  |  ||
    HQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNAL--TPTTM------PEGMGANIPMM
   350       360       370       380       390         400             410

       340        350       360       370       380       390       400
    QQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQK
          | |   |   |||   |  |  | |                 |        |       |
    GTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-----T
         420       430         440            450       460       470

      410       420        430            440            450        460
    SQGLDSRLQHVEDGVLSM-QVASARQTE-----SLESLLSKSQEH-----EQRLAALQG-RLEGLGSSEADQ
     |||    |       ||   ||    |          |   | |        |    |      ||||
    TQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETRG
         480          490       500       510       520       530       540

      470        480       490       500       510       520       530
    DGLASTVR-SLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSL
          ||  |  |      |  |         |     |   |
    ERVIDAVRFTLRQTISFPPRD--EWNDFNFDMDSRRNKQQRIKEEGE
          550       560         570       580     X

     540       550       560
    DNLKASVSQVEADLKMLRTAVDSLV
```

```
5. caa49535 (1-602)
   US-09-538-106-16 Sequence 16, Application US/09538106

 Sequence 16, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
```

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NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
 LENGTH: 586
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score     =      6  Optimized Score  =     78  Significance =  1.20
Residue Identity  =    19%  Matches          =    113  Mismatches   =   341
Gaps              =    132  Conservative Substitutions              =     0

                                                      X          10
                                                      MPS---AKQRGSKGGHGAASPS
                                                       ||        |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
            30        40        50        60        70        80        90

   20               30        40        50        60           70        80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
         100       110       120                130       140       150

          90       100       110       120       130                    140
    SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
      160              170         180       190       200       210

          150                160       170       180          190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQ---DLTEKAVKQGESEVSRIS
          |  |         || | |         |  |        |  ||   | |    | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDST----KNG------DG
   220       230       240        250       260       270

          210         220       230       240                 250        260
    EVLQKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQK
          ||        ||     |  |  |   |   |  | |   | |               | |   |
    TKRPFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQ
  280             290       300       310       320       330       340

           270       280        290       300       310         320
    RSQKEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRST--LQTMESDIYTEVRELV
      |      |        | ||    |       |    |         ||  |     |   |
    QQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMANI---------
      350       360       370       380       390       400

  330       340        350       360       370       380       390       400
    SLKQEQQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFE
               | |   |   |||   |  |  | |                 |        |       |
    --PMMGTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-
    410       420       430         440            450       460       470

           410       420        430            440       450       460
    ALQQKSQGLDSRLQHVEDGVLSM-QVASARQTE-----SLESLLSKSQEHEQRLAALQGRLEGLGSSEADQD
          |||    |       ||   ||    |          |   | ||         |    ||
    ----TTQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHE---FSSPSHLLRTPSS-----
              480          490       500       510          520

     470        480        490       500       510       520   X   530
    GLASTV-RSLGETQLVLYGD-VEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSL
      ||||     ||      | |    |     |   |              |
    --ASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
     530       540       550       560       570       580     X

     540       550       560       570
    DNLKASVSQVEADLKMLRTAVDSLVAYSVKIETNENNL

6. caa49535 (1-602)
   US-09-538-106-13 Sequence 13, Application US/09538106

 Sequence 13, Application US/09538106
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```
GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT:  YANG, ANNIE
 APPLICANT:  LODA, MASSIMO
 APPLICANT:  SIGNORETTI, SABINA
 APPLICANT:  CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 TITLE OF INVENTION:  RELATED THERETO
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE:  2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
  LENGTH: 641
  TYPE: PRT
  ORGANISM: Homo sapiens

Initial Score     =      6  Optimized Score  =     78  Significance =  1.20
Residue Identity  =    19%  Matches          =    113  Mismatches   =   341
Gaps              =    132  Conservative Substitutions              =     0

                                                      X          10
                                                      MPS---AKQRGSKGGHGAASPS
                                                       ||        |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
       80        90       100       110       120     X 130       140

   20               30        40        50        60           70        80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
    150       160       170       180                190       200       210

          90       100       110       120       130                    140
    SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
           220                230       240       250       260       270

          150                160       170       180          190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQ---DLTEKAVKQGESEVSRIS
          |  |         || | |         |  |        |  ||   | |    | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDST----KNG------DG
        280       290        300       310       320           330

          210         220       230       240                 250        260
    EVLQKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQK
          ||        ||     |  |  |   |   |  | |   | |               | |   |
    TKRPFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQ
       340             350       360      370       380       390       400

           270       280        290       300       310         320
    RSQKEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRST--LQTMESDIYTEVRELV
      |      |        | ||    |       |    |         ||  |     |   |
    QQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMANI---------
           410       420       430      440       450       460

  330       340        350       360       370       380       390       400
    SLKQEQQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFE
               | |   |   |||   |  |  | |                 |        |       |
    --PMMGTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-
         470       480       490             500       510       520

           410       420        430            440       450       460
    ALQQKSQGLDSRLQHVEDGVLSM-QVASARQTE-----SLESLLSKSQEHEQRLAALQGRLEGLGSSEADQD
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      |||    |        ||   ||    |          |   | ||          |    ||
----TTQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHE---FSSPSHLLRTPSS-----
     530          540        550       560       570          580

 470        480        490       500       510       520   X   530
GLASTV-RSLGETQLVLYGD-VEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSL
  ||||     ||      | |    |     |   |              |
--ASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
      590       600       610       620       630       640

 540       550       560       570
DNLKASVSQVEADLKMLRTAVDSLVAYSVKIETNENNL

7. caa49535 (1-602)
   US-09-538-106-19 Sequence 19, Application US/09538106

 Sequence 19, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 19
   LENGTH: 680
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score     =      6  Optimized Score  =     77  Significance =  1.20
Residue Identity  =    19%  Matches          =    111  Mismatches   =   343
Gaps              =    119  Conservative Substitutions              =     0

                                                  X          10
                                                  MPS---AKQRGSKGGHGAASPS
                                                   ||        |       |
GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
    120       130       140       150       160   X   170       180

20              30        40        50        60          70        80
EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGKSSSS
 | |               ||  |       |||         |     |     |  |
AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
 190       200       210       220                  230       240

      90        100       110       120       130                    140
SSASAAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
|        |  |        | |        |        |     |  |  ||               |
SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
250     260                270       280       290       300       310

      150                160       170         180       190      200
QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVL
      |  |         || | |         |  |        |  ||      | | |
VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDSA-KNG------DGTKR
     320       330        340       350       360        370

   210         220       230       240                 250        260
QKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQKRSQ
   ||        ||      |  |  |   |   |  | |   | |               | |   |   |
```

```
PFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQ
 380             390       400       410       420       430       440

    270       280        290       300       310       320       330
KEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
      |        | ||     |       |    |         ||  |  ||
HQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNAL--TPTTM------PEGMGANIPMM
     450       460       470       480       490                 500

   340        350       360       370       380       390       400
QQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQK
      | |   |   |||   |  |  | |                 |        |       |
GTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-----T
 510       520         530            540       550       560

  410       420        430            440            450        460
SQGLDSRLQHVEDGVLSM-QVASARQTE-----SLESLLSKSQEH-----EQRLAALQG-RLEGLGSSEADQ
 |||    |       ||   ||    |          |   | |        |    |      ||||
TQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHDFSSPPHLLRTPSGASTVSVGSSETRG
 570          580       590       600       610       620       630

  470        480       490       500           X      520       530
DGLASTVR-SLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSL
      ||  |  |      |  |         |     |   |
ERVIDAVRFTLRQTISFPPRD--EWNDFNFDMDSRRNKQQRIKEEGE
  640       650         660       670       680

 540       550       560
DNLKASVSQVEADLKMLRTAVDSLV

8. caa49535 (1-602)
   US-09-538-106-23 Sequence 23, Application US/09538106

 Sequence 23, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23
   LENGTH: 461
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score     =      5  Optimized Score  =     28  Significance =  0.00
Residue Identity  =    17%  Matches          =     33  Mismatches   =   131
Gaps              =     22  Conservative Substitutions              =     0

                                                  X       10        20
                                                  MPSAKQRGSKGGHGAASPSEKG
                                                  | | | | |          |
RRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDGTKRPFRQNTHGIQMTSIKKRRS-------PDDELL
     250       260       270       280       290  X    300

           30        40        50        60        70        80
AHPSGG-----ADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGKSSSSSSASAAA
  |  |          |      |  |        |  ||  |        |         | ||   |
YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQ--------HLLQKQTSMQSQSSYGNSSPP
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   310       320       330       340       350               360       370

  90       100       110       120       130       140       150       160
   AAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQK
        |     |       |     ||       |                          |   |
   LNKMNSMNKLPS--VSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
         380         390       400       410       420       430       440

         170        X      190       200       210       220       230
   VQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEILKDLSDGIHVVKDARERDFT
            |  || |  |
   HCTPPPPYPTDCSIVRIWQV
         450       460


9. caa49535 (1-602)
  US-09-538-106-17 Sequence 17, Application US/09538106

 Sequence 17, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 17
   LENGTH: 461
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score     =     5  Optimized Score   =    28  Significance =  0.00
Residue Identity =    17%  Matches           =    33  Mismatches   =   131
Gaps              =    22  Conservative Substitutions              =     0

                                                     X       10        20
                                                     MPSAKQRGSKGGHGAASPSEKG
                                                     | | | | |          |
   RRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRS-------PDDELL
        250       260       270       280       290  X    300

              30        40        50        60        70        80
   AHPSGG-----ADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKSSSSSSASAAA
     |  |          |      |  |        |  ||  |        |         | ||   |
   YLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQHQ--------HLLQKQTSIQSPSSYGNSSPP
   310       320       330       340       350               360       370

  90       100       110       120       130       140       150       160
   AAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQK
        |     |       |     ||       |                          |   |
   LNKMNSMNKLPS--VSQLINPQQRNALTPTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPLSMPSTS
         380         390       400       410       420       430       440

         170        X      190       200       210       220       230
   VQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEILKDLSDGIHVVKDARERDFT
            |  || |  |
   HCTPPPPYPTDCSIVRIWQV
         450       460

10. caa49535 (1-602)
```

```
    US-09-538-106-21 Sequence 21, Application US/09538106

 Sequence 21, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 21
   LENGTH: 483
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score     =     5  Optimized Score   =    79  Significance =  0.00
Residue Identity =    20%  Matches           =   115  Mismatches   =   310
Gaps              =   138  Conservative Substitutions              =     0

           10        20        30        40        50        60        70
   MPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGG
                                                      |  |    |         |
                                           MNFETSRCATLQYCPDPYIQ---------RFI
                                           X       10        20

         80        90       100            110              120       130
   GGGGGKSSSSSSASAAAAAAAAASSSASCSRRL-----GRALNFL-------FYLALVAAAAFSGWCVHHVLE
         |   |         | | |   |  |          ||           |      |        |
   ETPAHFSWKES-----YYRSAMSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPIELNFVDEPSENGATNKIE
        30             40        50        60        70        80        90

         140           150       160       170       180                190
   -EVQQVRRSHQDFS----RQREELGQGLQGVEQKVQSLQATFGTFESILRSSQHKQDLTEKA---------V
         |    | |     |   ||  |    |  |              ||      |  |
   ISMDCIRMQDSDLSDPMWPQYTNLG-LLNSMDQQIQ------------NGSSSTSPYNTDHAQNSVTAPSPY
          100       110        120                   130       140

          200       210       220       230       240       250       260
   KQGESEVSRISEVLQKLQNEILKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIFTEVQKRS
    |  |     |       |        | |          |    |     ||| |     ||      |
   AQPSSTFDALSPSPAIPSN----TDYPGPHSFDVSFQQSSTAKSAT-WTYSTEL-KKLYCQIA------KTC
 150       160           170       180       190         200

         270       280          290       300         310
   QKEINDM--KAKVASLEESEGNKQDLKA--LKEAVKEIQTSAKSRE--WDMEALRSTL---------QTMES
      |  |      |        |   ||    | ||       |||      |  | |         |  |
   PIQIKVMTPPPQGAVIRAMPVYK---KAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVED
 210       220       230          240       250       260       270

 320       330       340       350       360       370       380        390
   DIYTEVRELVSLKQEQQAFKEAADTERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDG
    |      ||     |        ||       |  |       |      ||       |         ||
   PITGRQSVLVPYEPPQ------VGTE------FTTVLYNFMCNSSCVGGMNRRPILIIVTL------ETRDG
  280       290                   300       310       320             330

         400       410                  420       430       440       450
   GFRHSEAFEALQQKSQGLD-------SRLQHVED----GVLSMQVASARQTESLESLLSKSQEHEQRLAALQ
          |||      | |        | | | |    |    |     |  |     |   |    |  |
   QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDAFRQNTHGIQMTSIKKRRSPDDE----LLYLP
        340       350       360       370       380       390           400
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         460       470       480       490       500       510       520
    GRLEGLGSSEADQDGLASTVRSLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARL
     |  |    |     |     || |    |     |  |           |||       |||
    VR--GRETYE----MLLKIKESL-ELMQYLPQHTIETYR-QQQQQQHQHLLQK------HLLSACFRNELVE
                 410        420       430        440             450

             530       540    X  550       560       570       580       590
    P------PQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAYSVKIETNENNLESAKGLLDDLRNDLDR
    |        |   | |   |   ||
    PRGEAPTQSDVFFRHSNPPN--HSVYP
   460       470         480  X


    LFVKV


11. caa49535 (1-602)
    US-09-538-106-14 Sequence 14, Application US/09538106

 Sequence 14, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 14
   LENGTH: 516
   TYPE: PRT
   ORGANISM: Homo sapiens


Initial Score    =      5  Optimized Score  =     74  Significance =  0.00
Residue Identity =    18%  Matches          =    106  Mismatches   =   334
Gaps             =    130  Conservative Substitutions              =     0

               X                   10        20            30        40
               MPSAKQ------------RGSKGGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPP
                |   |                       ||| ||      |             |  |
    MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQY
            10 X      20        30        40        50        60        70

       50        60        70        80          90       100       110
    PPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLA
              ||  ||               | || |      |     | |  |  |     ||      |
    TNLGLLNSMDQQ-IQN---------------GSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPA
          80                        90       100       110        120

      120       130       140       150       160       170           180
    LVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK-
            |   |      ||             ||   |     |    |    |       |      |
    IPSNTDYPG--PHSFDVSFQQSSTAKSATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKK
      130         140       150        160       170       180       190

          190       200       210                   220            230
    -QDLTEKAVKQGESEVSRISEVLQKLQNEIL------------KDLSDGIHVVKDARE-----RDFT-SLEN
        ||        | ||     |      |             |   |   |    |       ||  | |
    AEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYN
       200       210       220       230       240       250       260
```

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            240       250       260       270       280       290       300
    ------TVEERLTELTKSINDNIAIFTEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTSAK
           |          |         |  |   |        |      |   | ||  |     |
    FMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE--------ARICACPG--RDRKA-DEDSIRKQQVSD
     270       280       290       300               310          320

          310       320       330       340           350       360
    SREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAADTERLAL----QALTEKLLRSEESVSRLPEE
    |        |   |       |      | |          | | | |        | ||   ||
    STKNGDGTKRPFRQ------NTHGIQMTSIK-----KRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYL
    330       340             350            360       370       380

  370       380       390       400         410                 420
    IRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQ--KSQGLDS----------RLQHVEDGVLSMQ-VASA
         |  ||     |         |        |   | |  |           |  |       |  |
    PQHTIETYRQQQQQQH--------QHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALT
   390       400               410       420       430       440       450

   430       440       450       460       470       480       490       500
    RQTESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSLGETQLVLYGDVEELKRSVGELPSTV
      |                  |  |   ||    |    | |       |    |              | |
    PTTIPDGMGANIPMMGTHMPMA--GDMNGLSPTQALPPPL-SMPSTSHCTPPPPY----------PTDCSIV
         460       470         480       490        500                510

        X  510       520       530       540       550
    ESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRT
       |
    RIWQV
        X


12. caa49535 (1-602)
    US-09-538-106-20 Sequence 20, Application US/09538106

 Sequence 20, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 20
   LENGTH: 555
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score    =      5  Optimized Score  =     74  Significance =  0.00
Residue Identity =    18%  Matches          =    103  Mismatches   =   341
Gaps             =    122  Conservative Substitutions              =     0

                                                      X                   10
                                                      MPSAKQ------------RGSK
                                                       |   |
    MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPI
            10        20        30        40        50        60        70

            20            30        40        50        60        70
    GGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGK
           ||| ||      |             |  |            ||  ||               |
    ELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQ-IQN---------------GS
```

```
       80        90       100       110       120

 80          90       100       110       120       130       140
 SSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQR
 || |      |     | |  |  |     ||      |        |   |      ||
 SSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKSATWTYS
130       140       150          160       170         180       190

150       160       170           180         190       200       210
 EELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQNEIL--
  ||   |     |    |    |       |      |     ||        | ||     |      |
 TEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
    200       210       220       230       240       250       260

                220            230              240       250       260
 ----------KDLSDGIHVVKDARE-----RDFT-SLEN------TVEERLTELTKSINDNIAIFTEVQKRS
            |   |   |    |       ||  | |       |          |         |  |
 VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRR
  270       280       290       300       310       320       330

      270       280       290       300       310       320       330
 QKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
   |        |      |   | ||  |     |    |        |   |       |      | |
 CFE--------ARICACPG--RDRKA-DEDSIRKQQVSDSAKNGDGTKRPFRQ------NTHGIQMTSIK--
340                 350        360       370       380             390

    340           350       360       370       380       390       400
 QQAFKEAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEAL
         | | | |        | ||   ||            |  ||     |
 ---KRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH------QHLLQKQTSMQ
          400       410       420       430       440             450

      410       420       430       440                450       460
 QQKSQGLDSRLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLA---------ALQGRLEGLGSSEADQ
  | | |  |               |          |      |   |            |   ||    |
 SQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALP
    460       470       480       490       500       510       520

   470       480       490       500     X  510      520       530
 DGLASTVRSLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSLD
   | |       |    |              | |   |
 PPL-SMPSTSHCTPPPPY----------PTDCSIVRIWQV
   530       540                 550     X

 540       550
 NLKASVSQVEADLKMLRT
```

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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file s33377.res made by bshears on Wed 9 Jun 104 10:09:36-PDT.


Query sequence being compared:       s33377 (1-601)
Number of sequences searched:                    12
Number of scores above cutoff:                   12

      Results of the initial comparison of s33377 (1-601) with:
        File : /home/bshears/new.pep

    100-
       -
N      -
U    50-
M      -
B      -
E      -
R      -
       -
O      -
F    10-
       -
S      -                                                     *
E     5-                                                              *
Q      -
U      -
E      -                                            *
N      -
C      -
E      -
S     0---------------------------------------------------------------------------
      ||      |  |   |    | |      |      | |    |   |  |      |      |
SCORE 0|      1  |   2    | 2      3      4 |    5   |  5      6      7
STDEV -7        -6       -4        -3        -1        0


                              PARAMETERS

Similarity matrix       Unitary    K-tuple                     2
Mismatch penalty              1    Joining penalty            20
Gap penalty                1.00    Window size                32
Gap size penalty           0.05
Cutoff score                  0
Randomization group           0

                              SEARCH STATISTICS

Scores:                    Mean        Median        Standard Deviation
                              6             7              0.72

Times:                    CPU                        Total Elapsed
                      00:00:00.00                     00:00:00.00

Number of residues:                      6199
Number of sequences searched:              12
Number of scores above cutoff:             12

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                Init. Opt.
Sequence Name     Description                            Length Score Score  Sig. Frame
----------------------------------------------------------------------------------------
                    ****  1 standard deviation above mean ****
  1. US-09-538-106-24 Sequence 24, Application      389     7    61   1.39   0
  2. US-09-538-106-18 Sequence 18, Application      393     7    61   1.39   0
  3. US-09-538-106-15 Sequence 15, Application      448     7    66   1.39   0
  4. US-09-538-106-21 Sequence 21, Application      483     7    66   1.39   0
                    ****  0 standard deviation from mean ****
  5. US-09-538-106-23 Sequence 23, Application      461     6    58   0.00   0
  6. US-09-538-106-17 Sequence 17, Application      461     6    58   0.00   0
  7. US-09-538-106-22 Sequence 22, Application      586     6    79   0.00   0
  8. US-09-538-106-16 Sequence 16, Application      586     6    78   0.00   0
  9. US-09-538-106-13 Sequence 13, Application      641     6    78   0.00   0
 10. US-09-538-106-19 Sequence 19, Application      680     6    79   0.00   0
                    ****  1 standard deviation below mean ****
 11. US-09-538-106-14 Sequence 14, Application      516     5    75  -1.39   0
 12. US-09-538-106-20 Sequence 20, Application      555     5    76  -1.39   0


1. s33377 (1-601)
   US-09-538-106-24 Sequence 24, Application US/09538106

 Sequence 24, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 24
   LENGTH: 389
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score     =      7  Optimized Score  =     61  Significance =  1.39
Residue Identity =    18%  Matches          =     80  Mismatches   =   281
Gaps              =     65  Conservative Substitutions         =     0

           10        20        30        40    X   50        60        70
   MPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGG
                                                       |     ||    |
                                               MLYLENNAQTQFSEPQYTNLGLLNSMDQ
                                               X       10        20

         80         90      100       110       120       130       140
   GGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQ
       | || |      |     | |  |  |     ||      |        |   |      ||
   QIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKS
   30        40        50         60          70          80        90

        150       160       170           180         190       200
   DFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQ
          ||   |     |    |    |       |      |     ||        | ||     |
   ATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
     100        110       120       130       140       150       160

  210                  220       230       240       250       260
   NEIL------------KDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIFTEVQKRSQKEIND
      |             |   |   |    |      | |     | |      |         |    |
```

```
     PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----TVL-YNFMCNSSCVGGMNRRPILII--
      170       180       190       200             210       220       230

    270       280       290       300       310       320       330
     MKAKVASLEESEGNKQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFK-
            ||   |  | |                |  |    |              |      |     |
     -----VTLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDAFRQNTHGIQMTSIKKR
                   240       250       260       270       280       290

   340           350       360       370       380       390       400
     EAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQKSQ
        | | | |        | ||   ||            |  ||     |                | ||
     RSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH--------------QHLLQK--
       300       310       320       330       340                     350

     410          420       430       440 X     450       460       470
     GLDS---RLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAPAGALEGLGSSEADQDGLASTVRSLGE
      | |   |   ||               |     |
     HLLSACFRNELVEPRGEAPTQSDVFFRHSNPPNHSVYP
           360       370       380        X

      480       490
     TQLVLYGDVEELKRSV


2. s33377 (1-601)
   US-09-538-106-18 Sequence 18, Application US/09538106

 Sequence 18, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 18
   LENGTH: 393
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score     =      7  Optimized Score   =      61  Significance =  1.39
Residue Identity =     19%  Matches           =      83  Mismatches   =   278
Gaps              =     69  Conservative Substitutions                =     0

             10        20        30        40    X   50        60        70
     MPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGG
                                                         |     ||    |
                                                 MLYLENNAQTQFSEPQYTNLGLLNSMDQ
                                                 X       10        20

           80          90       100       110       120       130       140
     GGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQ
         | || |      |     | |  |  |     ||      |        |   |      ||
     QIQNGSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKS
     30        40        50         60          70          80        90

          150       160       170           180         190       200
     DFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQ
            ||   |     |    |    |       |      |     ||        | ||     |
     ATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAP
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       100        110       120       130       140       150       160

    210                   220       230       240       250       260
     NEIL------------KDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIFTEVQKRSQKEIND
        |             |   |   |    |      | |     | |      |         |    |
     PSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----TVL-YNFMCNSSCVGGMNRRPILII--
      170       180       190       200             210       220       230

    270       280        290         300       310       320        330
     MKAKVASLEESEGNKQDL-KALKEA--VKEIQTSAKSREWDMEALRSTLQTMESD-IYTEVRELVSLKQEQQ
            ||   |  | |     ||          |  |           |   |      |      |
     -----VTLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSTKNGDGTKRPFRQNTHGIQMTS
                   240       250       260       270       280       290

       340           350       360       370       380       390       400
     AFK-EAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQ
       |    | | | |        | ||   ||            |  ||     |                |
     IKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH--------------QHLL
       300       310       320       330       340                     350

         410          420       430       440 X     450       460       470
     QKSQGLDS---RLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAPAGALEGLGSSEADQDGLASTVR
     ||   | |   |   ||               |     |
     QK--HLLSACFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
           360       370       380       390  X

          480       490
     SLGETQLVLYGDVEELKRSV


3. s33377 (1-601)
   US-09-538-106-15 Sequence 15, Application US/09538106

 Sequence 15, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 15
   LENGTH: 448
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score     =      7  Optimized Score   =      66  Significance =  1.39
Residue Identity =     18%  Matches           =      93  Mismatches   =   296
Gaps              =    101  Conservative Substitutions                =     0

                X                   10        20            30        40
                MPSAKQ------------RGSKGGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPP
                 |   |                       ||| ||      |             |  |
     MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQY
             10 X      20        30        40        50        60        70

        50        60        70        80          90       100       110
     PPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLA
               ||  ||               | || |      |     | |  |  |     ||      |
     TNLGLLNSMDQQ-IQN---------------GSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPA
           80                        90       100       110        120
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  120       130       140       150       160       170           180
LVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK-
        |   |      ||             ||   |     |    |    |       |      |
IPSNTDYPG--PHSFDVSFQQSSTAKSATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKK
  130         140       150        160       170       180       190

      190       200       210                   220       230       240
-QDLTEKAVKQGESEVSRISEVLQKLQNEIL------------KDLSDGIHVVKDARERDFTSLENTVEERL
    ||        | ||     |      |             |   |   |    |      | |
AEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----
   200       210       220       230       240       250       260

      250       260       270       280        290         300       310
TELTKSINDNIAIFTEVQKRSQKEINDMKAKVASLEESEGNKQDL-KALKEA--VKEIQTSAKSREWDMEAL
| |      |         |    |         ||   |  | |     ||          |  |
TVL-YNFMCNSSCVGGMNRRPILII-------VTLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQ
       270       280              290         300       310       320

       320        330        340           350       360       370
RSTLQTMESD-IYTEVRELVSLKQEQQAFK-EAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEE
     |   |      |      |     |    | | | |        | ||   ||            |
QVSDSTKNGDGTKRPFRQNTHGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIET
    330       340       350       360       370       380       390

 380       390       400       410          420       430       440 X
LRQLKSDSHGPKEDGGFRHSEAFEALQQKSQGLDS---RLQHVEDGVLSMQVASARQTESLESLLSKSQEHE
 ||     |                | ||   | |   |   ||               |     |
YRQQQQQQH--------------QHLLQK--HLLSACFRNELVEPRRETPKQSDVFFRHSKPPNRSVYP
  400                     410         420       430       440       X

  450       460       470       480       490
QRLAPAGALEGLGSSEADQDGLASTVRSLGETQLVLYGDVEELKRSV

4. s33377 (1-601)
   US-09-538-106-21 Sequence 21, Application US/09538106

 Sequence 21, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 21
   LENGTH: 483
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score     =      7  Optimized Score    =     66  Significance =  1.39
Residue Identity =     18%  Matches            =     90  Mismatches   =   299
Gaps              =     97  Conservative Substitutions                =     0

                                                  X                   10
                                                  MPSAKQ------------RGSK
                                                   |   |
MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPI
        10        20        30        40        50        60        70
```

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        20            30        40        50        60        70
GGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGK
       ||| ||      |             |  |            ||  ||              |
ELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQ-IQN--------------GS
      80        90       100       110       120

80          90       100       110       120       130       140
SSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQR
|| |      |     | |  |  |     ||      |        |   |      ||
SSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKSATWTYS
130      140       150          160       170         180       190

150      160       170           180         190       200       210
EELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQNEIL--
 ||   |     |    |    |       |      |     ||        | ||     |      |
TEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
   200       210       220       230       240       250       260

               220       230       240       250       260       270
----------KDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIFTEVQKRSQKEINDMKAKVA
           |   |   |    |      | |     | |      |         |    |
VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFT-----TVL-YNFMCNSSCVGGMNRRPILII-------V
 270       280       290       300             310       320

   280       290       300       310       320       330        340
SLEESEGNKQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFK-EAADTE
 ||   |  | |                |  |    |              |      |     |    | |
TLETRDG--QVLGRRCFEARICACPGRDRKADEDSIRKQQVSDSAKNGDAFRQNTHGIQMTSIKKRRSPDDE
  330         340       350       360       370       380       390

      350       360       370       380       390       400       410
RLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQKSQGLDS--
 | |        | ||   ||            |  ||     |                | ||   | |
LLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH--------------QHLLQK--HLLSAC
  400       410       420       430                     440         450

       420       430       440 X     450       460       470       480
-RLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAPAGALEGLGSSEADQDGLASTVRSLGETQLVLY
 |   ||               |     |
FRNELVEPRGEAPTQSDVFFRHSNPPNHSVYP
      460       470       480  X

     490
GDVEELKRSV

5. s33377 (1-601)
   US-09-538-106-23 Sequence 23, Application US/09538106

 Sequence 23, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 23
   LENGTH: 461
   TYPE: PRT
   ORGANISM: Murine sp.
```

```
Initial Score     =      6  Optimized Score   =     58  Significance =  0.00
Residue Identity  =    18%  Matches           =     81  Mismatches   =   261
Gaps              =     89  Conservative Substitutions               =     0

                                                      X         10
                                                      MPS---AKQRGSKGGHGAASPS
                                                      ||         |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
            30        40        50        60        70        80        90

   20              30        40        50        60          70        80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
         100       110       120                130       140      150

          90       100       110       120       130                   140
    SSASAAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
      160              170         180       190       200      210

          150                160       170       180      190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVL
          |  |         || | |         |  |        |  ||     | | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDSA-KNG------DGTKR
   220       230       240        250       260      270              280

       210         220       230       240                250        260
    QKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQKRSQ
       ||        ||     |  |  |   |   |  | |   | |               | |   |  |
    PFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQ
               290       300       310       320      330       340

        270       280        290       300      310       320       330
    KEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
          |        | ||    |       |    |         ||  | ||
    HQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNAL--TPTTM------PEGMGANIPMM
   350       360       370       380      390         400             410

       340        350       360       370      380 X     390       400
    QQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQK
          | |   |   |||   |     |    |          |
    GTHMPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV
         420       430       440      450       460

      410       420       430
    SQGLDSRLQHVEDGVLSMQVASARQTE
```

6. s33377 (1-601)
US-09-538-106-17 Sequence 17, Application US/09538106

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Sequence 17, Application US/09538106
GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT:  YANG, ANNIE
 APPLICANT:  LODA, MASSIMO
 APPLICANT:  SIGNORETTI, SABINA
 APPLICANT:  CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 TITLE OF INVENTION:  RELATED THERETO
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE:  2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: 60/087,216
 PRIOR FILING DATE: 1998-05-29
 PRIOR APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: 1997-10-15
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
 LENGTH: 461
 TYPE: PRT
 ORGANISM: Homo sapiens

Initial Score     =      6  Optimized Score   =     58  Significance =  0.00
Residue Identity  =    18%  Matches           =     82  Mismatches   =   255
Gaps              =     99  Conservative Substitutions               =     0

                                                      X         10
                                                      MPS---AKQRGSKGGHGAASPS
                                                      ||         |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
            30        40        50        60        70        80        90

   20              30        40        50        60          70        80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
         100       110       120                130       140      150

          90       100       110       120       130                   140
    SSASAAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
      160              170         180       190       200      210

          150                160       170      180          190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQ---DLTEKAVKQGESEVSRIS
          |  |         || | |         |  |        |  ||   | |    | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDST----KNG------DG
   220       230       240        250      260       270

          210         220       230      240                 250        260
    EVLQKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQK
          ||        ||     |  |  |   |   |  | |   | |               | |   |
    TKRPFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQ
  280             290       300      310       320       330       340

           270       280       290       300       310         320
    RSQKEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRST--LQTMESDIYTEVRELV
      |      |        | ||    |       |    |         ||  |     |   |
    QQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANI--------
      350       360       370      380       390       400

  330       340        350      360       370       380  X    390       400
    SLKQEQQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFE
               | |   |   |||   |     |    |          |
    --PMMGTHMPMAGDMNGLSPTQALPPPLSMPSTSHCTPPPPYPTDCSIVRIWQV
    410       420       430      440       450       460

           410       420      430
    ALQQKSQGLDSRLQHVEDGVLSMQVASARQTE
```

7. s33377 (1-601)
US-09-538-106-22 Sequence 22, Application US/09538106

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Sequence 22, Application US/09538106
GENERAL INFORMATION:
 APPLICANT: MCKEON, FRANK
 APPLICANT:  YANG, ANNIE
 APPLICANT:  LODA, MASSIMO
 APPLICANT:  SIGNORETTI, SABINA
 APPLICANT:  CRUM, CHRISTOPHER
 TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
 TITLE OF INVENTION:  RELATED THERETO
 FILE REFERENCE: HMV-038.02
 CURRENT APPLICATION NUMBER: US/09/538,106
 CURRENT FILING DATE:  2000-03-29
 PRIOR APPLICATION NUMBER: 09/174,493
 PRIOR FILING DATE: 1998-10-15
```

```
PRIOR APPLICATION NUMBER: 60/087,216
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/062,076
PRIOR FILING DATE: 1997-10-15
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
  LENGTH: 586
  TYPE: PRT
  ORGANISM: Murine sp.

Initial Score     =      6  Optimized Score  =      79  Significance =  0.00
Residue Identity =     19%  Matches          =     113  Mismatches   =   339
Gaps              =    122  Conservative Substitutions             =     0

                                                    X          10
                                                    MPS---AKQRGSKGGHGAASPS
                                                     ||        |       |
  GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
          30        40        50        60        70        80        90

 20              30        40        50        60           70        80
  EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
   | |               ||  |       |||         |     |     |  |
  AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
       100       110       120                130       140       150

        90       100       110       120       130                    140
  SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
  |        |  |        | |        |        |     |  |  ||               |
  SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
    160              170         180       190       200       210

        150                160       170       180       190       200
  QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVL
        |  |         || | |         |  |        |  ||     | | |
  VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDSA-KNG------DGTKR
 220       230       240        250       260       270              280

     210         220       230       240                 250        260
  QKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQKRSQ
     ||        ||     |  |  |   |   |  | |   | |               | |   |   |
  PFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQ
             290       300       310       320       330       340

      270       280        290       300       310       320       330
  KEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
        |        | ||    |       |    |         ||  |  ||
  HQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNAL--TPTTM------PEGMGANIPMM
 350       360       370       380       390         400             410

     340        350       360       370       380       390       400
  QQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQK
        | |   |   |||   |  |  | |                 |        |       |
  GTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-----T
       420       430         440            450       460       470

    410       420        430       440                   450        460
  SQGLDSRLQHVEDGVLSM-QVASARQTESLESLLSK------------SQEHEQRLAPAGA-LEGLGSSEAD
   |||    |       ||   ||    |       |            |  |  |  | ||     ||||
  TQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHDFSSPPHLLR-TPSGASTVSVGSSETR
       480          490       500       510       520        530       540

      470        480       490       500       510       520       530
  QDGLASTVR-SLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSS
         ||  |  |      |  |         |     |   |
  GERVIDAVRFTLRQTISFPPRD--EWNDFNFDMDSRRNKQQRIKEEGE
         550       560         570       580     X

     540       550       560
  LDNLKASVSQVEADLKMLRTAVDSLV
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8. s33377 (1-601)
   US-09-538-106-16 Sequence 16, Application US/09538106

 Sequence 16, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 16
   LENGTH: 586
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score     =      6  Optimized Score  =      78  Significance =  0.00
Residue Identity =     19%  Matches          =     113  Mismatches   =   341
Gaps              =    131  Conservative Substitutions             =     0

                                                    X          10
                                                    MPS---AKQRGSKGGHGAASPS
                                                     ||        |       |
  GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
          30        40        50        60        70        80        90

 20              30        40        50        60           70        80
  EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
   | |               ||  |       |||         |     |     |  |
  AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
       100       110       120                130       140       150

        90       100       110       120       130                    140
  SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
  |        |  |        | |        |        |     |  |  ||               |
  SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
    160              170         180       190       200       210

        150                160       170       180          190       200
  QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQ---DLTEKAVKQGESEVSRIS
        |  |         || | |         |  |        |  ||   | |    | |
  VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDST----KNG------DG
 220       230       240        250       260       270

        210         220       230       240                 250        260
  EVLQKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQK
        ||        ||     |  |  |   |   |  | |   | |               | |   |
  TKRPFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQ
280             290       300       310       320       330       340

         270       280        290       300       310         320
  RSQKEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRST--LQTMESDIYTEVRELV
    |      |        | ||    |       |    |         ||  |     |   |
  QQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANI--------
    350       360       370       380       390       400

330       340        350       360       370       380       390       400
  SLKQEQQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFE
             | |   |   |||   |  |  | |                 |        |       |
  --PMMGTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-
  410       420       430         440            450       460       470
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           410       420        430            440       450       460
    ALQQKSQGLDSRLQHVEDGVLSM-QVASARQTE-----SLESLLSKSQEHEQRLAPAGALEGLGSSEADQDG
          |||    |       ||   ||    |          |   | ||    |   |    |
    ----TTQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHE-FSSPSHLLRTPSS-------
              480          490       500       510        520

     470        480        490       500       510       520  X    530
    LASTV-RSLGETQLVLYGD-VEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSLD
     ||||     ||      | |    |     |   |              |
    -ASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
    530       540       550       560       570       580     X

     540       550       560       570
    NLKASVSQVEADLKMLRTAVDSLVAYSVKIETNENNL

9. s33377 (1-601)
   US-09-538-106-13 Sequence 13, Application US/09538106

 Sequence 13, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
   LENGTH: 641
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score    =      6  Optimized Score =      78  Significance =  0.00
Residue Identity =    19%  Matches         =     113  Mismatches   =   341
Gaps             =    131  Conservative Substitutions              =     0

                                                      X          10
                                                      MPS---AKQRGSKGGHGAASPS
                                                       ||        |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
       80        90       100       110       120     X 130       140

   20              30        40        50        60           70        80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
    150       160       170       180                190       200       210

          90       100       110       120       130                    140
    SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
           220                230       240       250       260       270

          150                160       170       180          190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQ---DLTEKAVKQGESEVSRIS
          |  |         || | |         |  |        |  ||   | |    | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDST----KNG------DG
        280       290        300       310       320           330
```

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          210         220       230       240                 250        260
    EVLQKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQK
          ||        ||     |  |  |   |   |  | |   | |               | |   |
    TKRPFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQ
       340             350       360       370       380       390       400

           270       280        290       300       310         320
    RSQKEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRST--LQTMESDIYTEVRELV
      |      |        | ||    |       |    |         ||  |     |   |
    QQQHQHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTIPDGMGANI--------
           410       420       430       440       450       460

  330       340        350       360       370       380       390       400
    SLKQEQQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFE
               | |   |   |||   |  |  | |                 |        |       |
    --PMMGTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-
         470       480       490              500       510       520

           410       420        430            440       450       460
    ALQQKSQGLDSRLQHVEDGVLSM-QVASARQTE-----SLESLLSKSQEHEQRLAPAGALEGLGSSEADQDG
          |||    |       ||   ||    |          |   | ||    |   |    |
    ----TTQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHE-FSSPSHLLRTPSS-------
         530          540       550       560       570        580

     470        480        490       500       510       520  X    530
    LASTV-RSLGETQLVLYGD-VEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSLD
     ||||     ||      | |    |     |   |              |
    -ASTVSVGSSETRGERVIDAVRFTLRQTISFPPRDEWNDFNFDMDARRNKQQRIKEEGE
         590       600       610       620       630       640

     540       550       560       570
    NLKASVSQVEADLKMLRTAVDSLVAYSVKIETNENNL

10. s33377 (1-601)
    US-09-538-106-19 Sequence 19, Application US/09538106

 Sequence 19, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 19
   LENGTH: 680
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score    =      6  Optimized Score =      79  Significance =  0.00
Residue Identity =    19%  Matches         =     113  Mismatches   =   339
Gaps             =    122  Conservative Substitutions              =     0

                                                      X          10
                                                      MPS---AKQRGSKGGHGAASPS
                                                       ||        |       |
    GLLNSMDQQIQNGSSSTSPYNTDHAQNSVTAPSPYAQPSSTFDALSPSPAIPSNTDYPGPHSFDVSFQQSST
       120       130       140       150       160    X  170       180
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   20              30        40        50        60           70        80
    EKGA------HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQA---HGKGGHRGGGGGGGKSSSS
     | |               ||  |       |||         |     |     |  |
    AKSATWTYSTELKKLYCQIAKTCPIQIKVMTPPP---------QGAVIRAMPVYKKAEHVTEVVKRCPNHEL
     190       200       210       220                230       240

          90       100       110       120       130                    140
    SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQV-------------RRSH
    |        |  |        | |        |        |     |  |  ||               |
    SREFNEGQIAPPS-------HLIR--VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSC
  250       260              270       280       290       300       310

          150               160       170       180       190       200
    QDFSRQREEL---------GQGLQGVEQKVQSLQATFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVL
          |  |         || | |         |  |        |  ||     | | |
    VGGMNRRPILIIVTLETRDGQVL-GRRCFEARICACPGRDRKADEDSIRKQQVSDSA-KNG------DGTKR
         320       330        340       350       360        370

       210         220       230       240                 250        260
    QKLQNEILKDLSDGI--HVVKDARERDFTSLENTVEERLT--ELTK--------SINDNIAIFT-EVQKRSQ
       ||        ||     |  |  |   |   |  | |   | |               | |   |   |
    PFRQN------THGIQMTSIKKRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQ
     380             390       400       410       420       430       440

        270       280        290       300       310       320       330
    KEINDMKAKVASLEESEGN-KQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
          |        | ||    |       |    |         ||  |  ||
    HQHLLQKQTSMQSQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNAL--TPTTM------PEGMGANIPMM
         450       460       470       480       490               500

       340        350       360       370       380       390       400
    QQAFKEAADTERL-ALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQK
          | |   |   |||   |  |  | |                 |        |       |
    GTHMPMAGDMNGLSPTQALPPPL--SMPSTS-----HCTPPPPYPTDCSIVSFLARLGCSSCLDYF-----T
     510       520         530            540       550       560

      410       420        430       440                   450        460
    SQGLDSRLQHVEDGVLSM-QVASARQTESLESLLSK------------SQEHEQRLAPAGA-LEGLGSSEAD
     |||    |       ||   ||    |       |            |  |  |  | ||     ||||
    TQGLTTIYQ---IEHYSMDDLASLKIPEQFRHAIWKGILDHRQLHDFSSPPHLLR-TPSGASTVSVGSSETR
     570          580       590       600       610        620       630

        470        480       490       500         X       520       530
    QDGLASTVR-SLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSS
           ||  |  |      |  |         |     |   |
    GERVIDAVRFTLRQTISFPPRD--EWNDFNFDMDSRRNKQQRIKEEGE
       640       650         660       670       680

       540       550       560
    LDNLKASVSQVEADLKMLRTAVDSLV

11. s33377 (1-601)
    US-09-538-106-14 Sequence 14, Application US/09538106

 Sequence 14, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
```

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  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 14
   LENGTH: 516
   TYPE: PRT
   ORGANISM: Homo sapiens

Initial Score    =      5  Optimized Score  =     75  Significance = -1.39
Residue Identity =    18%  Matches          =    105  Mismatches   =   336
Gaps             =    127  Conservative Substitutions         =     0

               X                   10        20            30        40
               MPSAKQ------------RGSKGGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPP
                |   |                       ||| ||      |             |  |
    MSQSTQTNEFLSPEVFQHIWDFLEQPICSVQPIDLNFVDEPSEDGATNKIEISMDCIRMQDSDLSDPMWPQY
            10 X      20        30        40        50        60        70

       50        60        70        80          90       100       110
    PPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKSSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLA
              ||  ||               | || |      |     | |  |  |     ||      |
    TNLGLLNSMDQQ-IQN---------------GSSSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPA
          80                        90       100       110        120

      120       130       140       150       160       170           180
    LVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK-
            |   |      ||             ||   |     |    |    |       |      |
    IPSNTDYPG--PHSFDVSFQQSSTAKSATWTYSTEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKK
      130         140       150        160       170       180       190

          190       200       210                   220            230
    -QDLTEKAVKQGESEVSRISEVLQKLQNEIL------------KDLSDGIHVVKDARE-----RDFT-SLEN
        ||        | ||     |      |             |   |   |    |       ||  | |
    AEHVTEVVKRCPNHELSREFNEGQIAPPSHLIRVEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYN
       200       210       220       230       240       250       260

            240       250       260       270       280       290       300
    ------TVEERLTELTKSINDNIAIFTEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTSAK
           |          |         |  |   |        |      |   | ||  |     |
    FMCNSSCVGGMNRRPILIIVTLETRDGQVLGRRCFE--------ARICACPG--RDRKA-DEDSIRKQQVSD
     270       280       290       300               310          320

          310       320       330       340           350       360
    SREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAADTERLAL----QALTEKLLRSEESVSRLPEE
    |        |   |       |      | |          | | | |        | ||   ||
    STKNGDGTKRPFRQ------NTHGIQMTSIK-----KRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYL
    330       340             350            360       370       380

  370       380       390       400         410                 420
    IRRLEEELRQLKSDSHGPKEDGGFRHSEAFEALQQ--KSQGLDS----------RLQHVEDGVLSMQVASAR
         |  ||     |         |        |   | |  |           |  |       |
    PQHTIETYRQQQQQQH--------QHLLQKQTSIQSPSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALT
   390       400               410       420       430       440       450

  430       440       450       460       470       480       490       500
    QTESLESLLSKSQEHEQRLAPAGALEGLGSSEADQDGLASTVRSLGETQLVLYGDVEELKRSVGELPSTVES
     |                   ||   ||    |    | |       |    |              | |
    PTTIPDGMGANIPMMGTHMPMAGDMNGLSPTQALPPPL-SMPSTSHCTPPPPY----------PTDCSIVRI
         460       470       480       490        500                 510

      X   510       520       530       540       550
    LQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRT
     |
    WQV
      X

12. s33377 (1-601)
    US-09-538-106-20 Sequence 20, Application US/09538106

 Sequence 20, Application US/09538106
 GENERAL INFORMATION:
  APPLICANT: MCKEON, FRANK
```

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  APPLICANT:  YANG, ANNIE
  APPLICANT:  LODA, MASSIMO
  APPLICANT:  SIGNORETTI, SABINA
  APPLICANT:  CRUM, CHRISTOPHER
  TITLE OF INVENTION: CELL REGULATORY GENES, ENCODED PRODUCTS, AND USES
  TITLE OF INVENTION:  RELATED THERETO
  FILE REFERENCE: HMV-038.02
  CURRENT APPLICATION NUMBER: US/09/538,106
  CURRENT FILING DATE:  2000-03-29
  PRIOR APPLICATION NUMBER: 09/174,493
  PRIOR FILING DATE: 1998-10-15
  PRIOR APPLICATION NUMBER: 60/087,216
  PRIOR FILING DATE: 1998-05-29
  PRIOR APPLICATION NUMBER: 60/062,076
  PRIOR FILING DATE: 1997-10-15
  NUMBER OF SEQ ID NOS: 53
  SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 20
   LENGTH: 555
   TYPE: PRT
   ORGANISM: Murine sp.

Initial Score     =      5  Optimized Score  =     76  Significance = -1.39
Residue Identity =     18%  Matches          =    105  Mismatches   =   338
Gaps              =    123  Conservative Substitutions              =     0

                                                      X                   10
                                                      MPSAKQ------------RGSK
                                                       |   |
    MNFETSRCATLQYCPDPYIQRFIETPAHFSWKESYYRSAMSQSTQTSEFLSPEVFQHIWDFLEQPICSVQPI
            10        20        30        40        50        60        70

            20            30        40        50        60        70
    GGHGAASPSEKGA----HPSGGADDVAKKPPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGK
           ||| ||      |             |  |            ||  ||               |
    ELNFVDEPSENGATNKIEISMDCIRMQDSDLSDPMWPQYTNLGLLNSMDQQ-IQN---------------GS
          80        90       100       110       120

    80          90       100       110       120       130       140
    SSSS--SSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFSGWCVHHVLEEVQQVRRSHQDFSRQR
    || |      |     | |  |  |     ||      |        |   |      ||
   SSTSPYNTDHAQNSVTAPSPYAQPS-STFDAL--SPSPAIPSNTDYPG--PHSFDVSFQQSSTAKSATWTYS
   130       140       150          160       170         180       190

   150       160       170           180         190       200       210
    EELGQGLQGVEQKVQSLQATFGT----FESILRSSQHK--QDLTEKAVKQGESEVSRISEVLQKLQNEIL--
     ||   |     |    |    |       |      |     ||        | ||     |      |
    TEL-KKLYCQIAKTCPIQIKVMTPPPQGAVIRAMPVYKKAEHVTEVVKRCPNHELSREFNEGQIAPPSHLIR
       200       210       220       230       240       250       260

                   220            230              240       250       260
    ----------KDLSDGIHVVKDARE-----RDFT-SLEN------TVEERLTELTKSINDNIAIFTEVQKRS
               |   |   |    |       ||  | |       |          |         |  |
    VEGNSHAQYVEDPITGRQSVLVPYEPPQVGTEFTTVLYNFMCNSSCVGGMNRRPILIIVTLETRDGQVLGRR
     270       280       290       300       310       320       330

         270       280       290       300       310       320       330
    QKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTSAKSREWDMEALRSTLQTMESDIYTEVRELVSLKQE
      |        |      |   | || |     |    |        |   |       |      | |
    CFE--------ARICACPG--RDRKA-DEDSIRKQQVSDSAKNGDGTKRPFRQ------NTHGIQMTSIK--
   340                 350        360       370       380             390

       340           350       360       370       380       390       400
    QQAFKEAADTERLAL----QALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGPKEDGGFRHSEAFEAL
            | | | |        | ||   ||            |  ||     |
    ---KRRSPDDELLYLPVRGRETYEMLLKIKESLELMQYLPQHTIETYRQQQQQQH------QHLLQKQTSMQ
             400       410       420       430       440             450

         410                 420       430       440       450       460
    QQKSQGLDS----------RLQHVEDGVLSMQVASARQTESLESLLSKSQEHEQRLAPAGALEGLGSSEADQ
     | | |  |           |  |       |      |   |               ||   ||    |
    SQSSYGNSSPPLNKMNSMNKLPSVSQLINPQQRNALTPTTMPEGMGANIPMMGTHMPMAGDMNGLSPTQALP
       460       470       480       490       500       510       520

       470       480       490       500   X   510       520       530
    DGLASTVRSLGETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQAQAARLPPQDFLDRLSSLD
      | |       |    |              | |   |
    PPL-SMPSTSHCTPPPPY----------PTDCSIVRIWQV
      530       540                 550    X

     540       550
    NLKASVSQVEADLKMLRT
```